

REMARKS

Reconsideration and allowance are respectfully requested.

Claims 91-105 are now pending, with claim 91 being the sole independent claim.

Applicants have corrected the cross-reference to related applications section on page 1, lines 1-2, to correct an erroneously made priority claim and to reflect properly that the present application is a continuation of PCT/US99/06047, which claims the benefit of U.S. Provisional Application No. 60/078,948. No petition and fee is believed due, since the present application was filed prior to November 29, 2000.

A substitute Sequence Listing is filed simultaneously herewith. As explained further in the Remarks accompanying this substitute Sequence Listing, in SEQ ID NO:12, a 351 amino acid sequence (encoded by nucleotides 131-1186 of SEQ ID NO:11) replaces the originally-filed 339 amino acid sequence (encoded by nucleotides 167-1186 of SEQ ID NO:11).

A substitute Figure 2A-2B is submitted herewith. Figure 2 as originally filed contained the sequence of originally-filed SEQ ID NO:12, i.e., the 339 amino acid sequence mentioned above. The attached substitute Figure 2A-2B now contains the 351 amino acid sequence of SEQ ID NO:12 submitted in the substitute Sequence Listing filed simultaneously herewith.

A substitute Figure 3A-3B is submitted herewith. Figure 3 as originally filed erroneously contained a partial amino acid sequence of 344 residues for SEQ ID NO:18. The attached substitute Figure 3A-3B now contains, for SEQ ID NO:18, the 388 amino acid sequence of SEQ ID NO:18 as originally filed. Further basis for this amendment is found in the specification at page 3, lines 21-22, which describes Figure 3 as containing SEQ ID NO:18.

A currently amended Table 5, of Example 4, is submitted to correct the following errors in the original Table 5: 1) the original percent identities were erroneously based on a comparison to the Arabidopsis delta-1 cyclin of GI No. 1076311, instead of to the highly similar Arabidopsis delta-1 cyclin of GI No. 3915635 (SEQ ID NO:30) as stated at page 20, lines 8-13 of the specification; 2) the amino acid sequence of the currently amended SEQ ID NO:12 is used; and 3) for some sequences of the original Table 5, a "period" was used in the amino acid sequence to correspond to the stop codon; in the currently amended Table 5, all amino acid sequences used are as presented in the currently amended Sequence Listing, i.e., no periods are used to indicate the end of the protein.

A currently amended Table 7, of Example 5, is submitted to properly list the percent identity of the amino acid sequence of SEQ ID NO:18 when compared to the Nicotiana tabacum cyclin delta-2 protein (SEQ ID NO:31). The basis for this

correction is page 22, lines 5-8 and lines 27-30 of the specification. In Table 7 as originally filed, the percent identities were erroneously calculated using a partial amino acid sequence of 344 residues for SEQ ID NO:18. A spelling error in the title of Table 7 is also corrected.

No new matter is believed to have been added.

Turning now to the Office Action mailed January 2, 2003:

Regarding the combined Section 101 (utility) and Section 112, 1st paragraph (how to use) rejections, Applicants submit the following as rebuttal arguments:

First, reference is made to Appendix A, attached hereto. Appendix A contains a BLASTX analysis indicating the result shown in Table 4 of the instant specification, namely, an E-115 probability of the sequence similarity between the polypeptide encoded by SEQ ID NO:11 and the Arabidopsis cyclin delta-1 having occurred by chance, as well as the top ten BLASTX hits, with probabilities ranging from E-115 to 8E-44, are to delta cyclins from Arabidopsis, Nicotiana tabacum, and Chenopodium rubrum.

Second, Clustal comparison of SEQ ID NO:12 to the Arabidopsis cyclin delta-1 (SEQ ID NO:30) is 57% as now reflected in amended Table 5. Additionally, a pairwise Clustal alignment of the amended SEQ ID NO:12 and SEQ ID NO:30 (Arabidopsis cyclin delta-1) is given in Appendix B.¹ The pairwise alignment shows three regions of sequence identity: 1) Region A, containing amino acids 1-60 of SEQ ID NO:12, has 32% sequence identity to SEQ ID NO:30; 2) Region B, containing amino acids 61-248, has 77% sequence identity to SEQ ID NO:30; and 3) Region C, containing amino acids 249-351, has 32% sequence identity to SEQ ID NO:30. Consequently, the sequence comparison of SEQ ID NO:12 to SEQ ID NO:30 indicates a large central region of high sequence identity (77%), between smaller amino and carboxyl-terminal regions of lower sequence identity (32% each).

Third, in the amino-terminal Region A, there is the presence of an Rb-binding domain, L-X-C-X-E, that is conserved among delta cyclins. See Soni, B. et al. (1995) Plant Cell 7(1):85-103, cited in the previously submitted IDS).

In view of the foregoing, Applicants submit that one of skill in the art would expect SEQ ID NO:12 to represent a functional cyclin delta-1 protein, and therefore,

¹ In Appendix B the numbering of the consensus sequence is given below the sequence alignment. The numbering of each sequence is given to the left of each row, and to the right of the last row. Positions that contain identical amino acids in each sequence are indicated with an asterisk. Amino-terminal sequence from a related clone, scr1c.pk003.j21, is given below the sequence alignment.

respectfully request withdrawal of the combined Section 101 and Section 112, 1st paragraph rejection.

Applicants further wish to note the following. The contig of SEQ ID NO:11 encodes a protein of 351 amino acids. Amino acids 11-351 (97% of the protein) are from the cDNA insert in clone sr1.pk0001.g5, and amino acids 1-10 are from the EST sequence of clone sah1c.pk003.i7. After the filing date of the instant application, Applicants sequenced the entire cDNA insert of sah1c.pk003.i7 and determined that this clone represented a different, but highly homologous, sequence to that of sr1.pk0001.g5. Consequently, the joining of sequences from clones sr1.pk0001.g5 and sah1c.pk003.i7 created an artificial contig sequence. A different clone, scr1c.pk003.j21, from the proprietary database was found to represent the authentic 5' end of the gene represented by clone sr1.pk0001.g5. Consequently, the authentic amino-terminus for the protein 97% encoded by sr1.pk0001.g5 can be obtained from clone scr1c.pk003.j21. The authentic amino-terminus is shown in Appendix B, below the sequence alignment. Instead of the 10 amino acids, MNAEPPLPPA, from the contig in SEQ ID NO:11, the authentic protein should have the following eight amino acids, MNAESPPG, at the amino-terminus. Because these two short sequences are very similar (six amino acids are identical), and because, in general, alterations of the N-terminal and C-terminal portions of a protein molecule would also not be expected to alter the activity of the protein (see the specification, page 6, lines 21-23), Applicants contend that one of skill in the art would expect the artificial sequence of SEQ ID NO:12 to represent a functional cyclin delta-1 protein.

Regarding the Section 112, 1st paragraph written description rejection, Applicants respectfully traverse.

Applicants submit that the specification discloses to one of ordinary skill in the art a representative number of polynucleotides encoding a polypeptide having cyclin delta activity, wherein the amino acid sequence of the polypeptide and the amino acid sequence of SEQ ID NO:12 have at least 80% sequence identity based on the Clustal alignment method.

The specification at page 6, lines 13-25, discloses alterations in nucleotide sequence that are not expected to alter functionality, such as alterations that produce a chemically equivalent amino acid at a given site or alterations in the N- or C-terminal portions. Also in the specification, at page 4, Table 4, the result (pLog = 115) of a BLASTX analysis is given for comparison of the protein encoded by SEQ ID NO:11 and the Arabidopsis cyclin delta-1 (SEQ ID NO:30). The sequence alignment from that BLASTX analysis is presented as Appendix C. In the alignment of Appendix C, the position of forty conservative amino acid changes are noted with "plus" signs. Thus, from the foregoing, the skilled artisan would immediately

understand the specification to disclose a representative number of polynucleotide sequences, having different nucleotide substitutions, that encode polypeptides having cyclin delta-1 enzyme activity but that vary from the 351 amino acids encoded by SEQ ID NO:11.

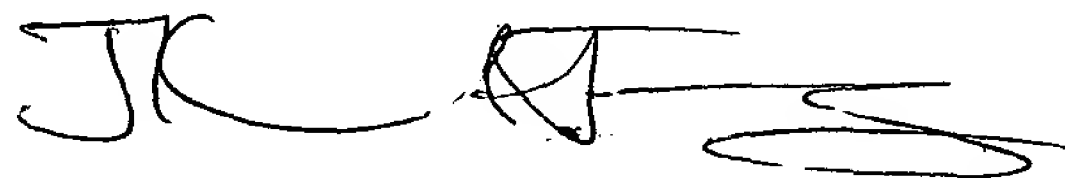
Withdrawal of the Section 112, 1st paragraph written description rejection is therefore respectfully requested.

Applicants believe the foregoing to be responsive to each point raised in the Office Action. A Notice of Allowance is respectfully requested.

Please charge any fees or credit any overpayment of fees which are required in connection herewith to Deposit Account No. 04-1928 (E. I. du Pont de Nemours and Company).

Applicants' undersigned may be reached at the below-listed numbers.

Respectfully submitted,



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Dated: 2 July 2003

Enclosures: Appendices A, B & C
Substitute Figures 2A-2B and 3A-3B

APPENDIX A

BLASTX 2.0.6 [Sept-16-1998]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= sahlc.pk003.i7 2/16/99 no filter, Becky
(2259 letters)

Database: /blast/data/2.0/2/nr
356,412 sequences; 108,900,843 total letters

Searching.....done

Sequences producing significant alignments:	Score (bits)	E Value	N	plog
gi 3915635 sp P42751 CGD1_ARATH CYCLIN DELTA-1 >gi 2995130 g...	357	e-115	4	115.00
gi 2194121 (AC002062) Strong similarity to Arabidopsis cycli...	357	e-113	3	113.00
gi 1076311 pir S51650 cyclin delta-1 - Arabidopsis thaliana	277	1e-91	4	
gi 4160300 gnl PID e1370827 (AJ011893) cyclin D3.1 protein [...	197	4e-49	1	
gi 4160298 gnl PID e1370825 (AJ011892) cyclin D2.1 protein [...	193	7e-48	1	
gi 3915637 sp P42753 CGD3_ARATH CYCLIN DELTA-3 >gi 2995134 g...	186	6e-46	2	
gi 1076313 pir S51652 cyclin delta-3 - Arabidopsis thaliana	186	6e-46	2	
gi 2911046 gnl PID e1253334 (AL021961) cyclin delta-3 [Arabi...	186	8e-46	2	
gi 1770190 gnl PID e290219 (Y10162) cyclin-D like protein [C...	123	1e-45	3	
gi 1076312 pir S51651 cyclin delta-2 - Arabidopsis thaliana	169	8e-44	3	

>gi|3915635|sp|P42751|CGD1_ARATH CYCLIN DELTA-1 >gi|2995130|gnl|PID|e1284155 (X83369)
cyclin delta-1
[Arabidopsis thaliana]
Length = 335

Score = 38.2 bits (77), Expect(4) = e-115
Identities = 199/307 (64%), Positives = 239/307 (77%)

Query: 161 LLMSVSCLSDYDLLCGEDSSGILSGESPECSFSDIDSSP 277
L MSVS +D DL CGEDS + + S S++DS P
Sbjct: 10 LHMSVSFSNDMDLFCGEDSGVFSGESTVDFSSSEVDSWP 48

Score = 357 bits (774), Expect(4) = e-115
Identities = 181/268 (67%), Positives = 216/268 (80%)

Query: 311 SIAFIEHERNFVPGFEYLSRFQSRSLDANAREESVGWILKVHAYYGFQPLTAYLAVNYM 490
SIA FIE ER+FVPG +YLSRFQ+RSLDA+ARE+SV WILKV AYY FQPLTAYLAVNYM
Sbjct: 51 SIACFIEDERHFVPGHDYLSRFQTRSLDASAREDSVAWILKVQAYYNFQPLTAYLAVNYM 110

Query: 491 DRFLDSRRLPETNGWPLQLVSVACLSLAAKMEEPLVPSLLDLQIEGAKYIFEPRTIRME 670
DRFL +RRLPET+GWP+QL++VACLSLAAKMEE LVPSL D Q+ G KY+FE +TI+RME
Sbjct: 111 DRFLYARRLPETSGWPMQLLAVACLSLAAKMEEILVPSLFDQVAGVKYLFEAKTIKME 170

Query: 671 LLVLGVLDWRLRSVTPLCFLAFFACKVDSTGTFFIRFLISRATEIIVSNIQEASFLAYWPS 850
LLVL VLDWRLRSVTP F++FFA K+D +GTF+ F IS ATEII+SNI+EASFL YWPS
Sbjct: 171 LLVLSVLDWRLRSVTPFDFISFFAYKIDPSGTFLGFFISHATEIILSNIKEASFLEYWPS 230

Query: 851 CIAAAAILTAANEIPNWSVV 910
IAAAAIL ANE+P+ S V
Sbjct: 231 SIAAAAILCVANELPSLSSV 250

APPENDIX A (continued)

Score = 53.3 bits (110), Expect(4) = e-115
Identities = 31/68 (45%), Positives = 43/68 (62%)

Query: 917 ENAESWCEGLRKEKVIQCYQLMQELVINNNQRKLP 1021
E+ E+WC+GL KEK++ CY+LM+ + I NN+ P
Sbjct: 255 ESPETWCDGLSKEKIVRCYRLMKAMAIENNRLNTP 289

Score = 29.0 bits (57), Expect(4) = e-115
Identities = 14/33 (42%), Positives = 17/33 (51%)

Query: 1073 SSTVSSFSSSSSTSFSLCKRRKLNRLWVDDK 1171
S SS + S S CKRRKL+ WV D+
Sbjct: 298 SVRASSTLTRPSDESSSPCKRRKLSGYSWVGDE 330

>gi|2194121 (AC002062) Strong similarity to Arabidopsis cyclin delta-1
(gb|ATCD1). EST gb|ATTS4338 comes from this gene.
[Arabidopsis thaliana]
Length = 339

Score = 38.2 bits (77), Expect(3) = e-113
Identities = 208/336 (61%), Positives = 255/336 (74%)

Query: 161 LLMSVSCLSDYDLLCGEDSSGILSGESPECSFSDIDSSP 277
L MSVS +D DL CGEDS + + S S++DS P
Sbjct: 10 LHMSVSFSNDMDLFCGEDSGVFSGESTVDFSSSEVDSWP 48

Score = 357 bits (774), Expect(3) = e-113
Identities = 190/297 (63%), Positives = 232/297 (77%)

Query: 311 SIAFIEHERNFVPGFEYLSRFQSRSLDANAREESVGWILKVHAYYGFQPLTAYLAVNYM 490
SIA FIE ER+FVPG +YLSRFQ+RSLDA+ARE+SV WILKV AYY FQPLTAYLAVNYM
Sbjct: 51 SIACFIEDERHFVPGHDYLSRFQTRSLDASAREDSVAWILKVQAYYNFQPLTAYLAVNYM 110

Query: 491 DRFLDSRRLPETNGWPLQLVSVACLSLAAKMEEPLVPSLLDLQIEGAKYIFEPRTIRRME 670
DRFL +RRLPET+GWP+QL++VACLSLAAKMEE LVPSL D Q+ G KY+FE +TI+RME
Sbjct: 111 DRFLYARRLPETSGWPMQLLAVACLSLAAKMEEILVPSLFDQVAGVKYLFEAKTIKRME 170

Query: 671 LLVLGVLDWRLRSVTPLCFLAFFACKVDSTGTFFIRFLISRATEIIVSNIQEASFLAYWPS 850
LLVL VLDWRLRSVTP F++FFA K+D +GTF+ F IS ATEII+SNI+EASFL YWPS
Sbjct: 171 LLVLSVLDWRLRSVTPFDFFISFFAYKIDPSGTFGLGFFISHATEIILSNIKEASFLEYWPS 230

Query: 851 CIAAAAILTAANEIPNWSVV 910
IAAAAIL ANE+P+ S V
Sbjct: 231 SIAAAAILCVANELPSLSSV 250

Score = 56.5 bits (117), Expect(3) = e-113
Identities = 40/97 (41%), Positives = 59/97 (60%)

Query: 917 ENAESWCEGLRKEKVIQCYQLMQELVINNNQRKLP LLKVLPLQRLVTTRTRMRSSSTVSSFS 1096
E+ E+WC+GL KEK++ CY+LM+ + I NN+ P + ++ V + + + S
Sbjct: 255 ESPETWCDGLSKEKIVRCYRLMKAMAIENNRLNTPKVIKLRVSVRASSTLTRPSDESSF 314

Query: 1097 SSSS 1108
SSSS
Sbjct: 315 SSSS 318

Score = 36.8 bits (74), Expect = 1.0
Identities = 17/33 (51%), Positives = 21/33 (63%)

Query: 1073 SSTVSSFSSSSSTSFSLCKRRKLNRLWVDDK 1171
SST++ S SS S S CKRRKL+ WV D+
Sbjct: 302 SSTLTRPSDESSFSSSPCKRRKLSGYSWVGDE 334

APPENDIX A (continued)

>gi|1076311|pir||S51650 cyclin delta-1 - Arabidopsis thaliana
Length = 334

Score = 38.2 bits (77), Expect(4) = 1e-91
Identities = 174/312 (55%), Positives = 215/312 (68%)

Query: 161 LLMSVSCSLSDYDLLCGEDSSGILSGESPECSFSDIDSSP 277
L MSVS +D DL CGEDS + + S S++DS P
Sbjct: 10 LHMSVSFSNDMDLFCGEDSGVFSGESTVDFSSSEVDSWP 48

Score = 277 bits (599), Expect(4) = 1e-91
Identities = 156/273 (57%), Positives = 192/273 (70%)

Query: 311 SIASFIEHERNFVPGFEYLSRFQSRSLDANAREESVGWILKVHAYYGFQPLTAYLAVNYM 490
SIA FIE ER FVPG +YLSRFQ+RSLDA+ARE+SV WILKV AYY FQPL+AYLAVNYM
Sbjct: 51 SIACFIEDERTFVPGHDYLSRFQTRSLDASAREDSVAWILKVQAYYNFQPLSAYLAVNYM 110

Query: 491 DRFLDSRRLPETNGWPLQLVSVACLSLAAKMEEPLVPSLLDLQIEGAKYIFEPRTIRRME 670
DRFL +RRLPET+GWP+QL++VACLSLAAKMEE LVPSL D Q+ G KY+FE +TI+RME
Sbjct: 111 DRFLYARRLPETSGWPMQLLAVACLSLAAKMEEILVPSLFDQVAGVKYLF EAKTIKRME 170

Query: 671 LLVLGVLDWRLRSVTPLCFLAFFACKVDSTGTGFIRFLISRATEIIVSNIQEASFLAYWPS 850
LLVL VLDWRLRSVTP F++FFA K+D F L I+ + + + + S
Sbjct: 171 LLVLSVLDWRLRSVTPFDFFISFFAYKIDLRVPFSGSLSPMLQSILSNIKEASFLEYWPSS 230

Query: 851 CIAAAAILTAANEIPNWSVVKPENA 925
AAA + A SVV P +
Sbjct: 231 IAAAILCVANELPSLSSVVNPHES 255

Score = 53.3 bits (110), Expect(4) = 1e-91
Identities = 31/68 (45%), Positives = 43/68 (62%)

Query: 917 ENAESWCEGLRKEKVIQCYQLMQELVINNNQKLP 1021
E+ E+WC+GL KEK++ CY+LM+ + I NN+ P
Sbjct: 254 ESPETWCDGLSKEKIVRCYRLMKAMAIENNRLNTP 288

Score = 29.0 bits (57), Expect(4) = 1e-91
Identities = 14/33 (42%), Positives = 17/33 (51%)

Query: 1073 SSTVSSFSSSSSTSFSLSCKRRKLNNRLWVDDK 1171
S SS + S S CKRRKL+ WV D+
Sbjct: 297 SVRASSTLTRPSDESSSPCKRRKLSGYSWVGDE 329

>gi|4160300|gnl|PID|e1370827 (AJ011893) cyclin D3.1 protein [Nicotiana tabacum]
Length = 373

Score = 197 bits (425), Expect = 4e-49
Identities = 90/210 (42%), Positives = 126/210 (59%)

Query: 362 YLSRFQSRSLDANAREESVGWILKVHAYYGFQPLTAYLAVNYMDRFLDSRRLPETNGWPL 541
+ + FQ SL +AR +SV WILKV+ YYGF LTA LA+NY DRFL S + W +
Sbjct: 89 WFNSFQDDSLCSARVDSVEWILKVNGYGFSAITAVLAINYFDRFLTSLHYQKDKPWWI 148

Query: 542 QLVSVACLSLAAKMEEPLVPSLLDLQIEGAKYIFEPRTIRRMELLVLGVLDWRLRSVTPL 721
QL +V CLSLAAK+EE VP LLD Q+E AKY+FE +TI+RMELLVL L WR+ VTPL
Sbjct: 149 QLAAVTCLSLAAKVEETQVPLLLDFQVEDAKYVFEAKTIQRMELLVLSSLKWRMNPVTPL 208

Query: 722 CFLAFFACKVDSTGTGFIRFLISRATEIIVSNIQEASFLAYWPS CIAAAAILTAANEIPNW 901
FL ++ + R +++S + + F+ Y PS +A A +L +++
Sbjct: 209 SFLDHIIRRLGLRNNIHWEFLRCENLLLSIMADCRFVRYMPSVLATAIMLHVHQVEPC 268

Query: 902 SVVKPENAESWCEGLRKEKVIQCYQLMQEL 991
+ V +N + KEKV C++L+ E+
Sbjct: 269 NSVDYQNQLLGVKINKEKVNNCFELISEV 298

APPENDIX A (continued)

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>gi|4160298|gnl|PID|e1370825 (AJ011892) cyclin D2.1 protein [Nicotiana tabacum]
Length = 354

Score = 193 bits (416), Expect = 7e-48
Identities = 83/193 (43%), Positives = 127/193 (65%)

Query: 314 IASFIEHERNFVPGFEYLSRFQSRSLDANAREESVGVILKVHAYYGFQPLTAYLAVNYMD 493
      ++ ++ E F+P +Y+ R +S LD + R+E++ WILK H +YGF L+ L++NY+D
Sbjct: 66 LSFMVQREMEFLPKDDYVERLRSGDLDSVRKEALDWILKAHMHYGFGLSFCLSINYLD 125

Query: 494 RFLDSRRLPETNGWPLQLVSVACLSLAAKMEEPLVPSLLDLQIEGAKYIFEPRTIRRMEL 673
      RFL LP + W +QL++VACLSLAAKMEE VP +DLQ+ K++FE +TI+RMEL
Sbjct: 126 RFLSLYELPRSKTWTVQLLAVACLSLAAKMEEINVPLTVDLQVGDPKFVFEKGKTIQRMEL 185

Query: 674 LVLGVLDWRLRSVTPLCFLAFFACKVDSTGTFRFLISRATEIIVSNIQEASFLAYWPSC 853
      LVL L WR+++ TP F+ +F K++ R LIS + ++I+S I+ FL + S
Sbjct: 186 LVLSTLKWARMQAYTPYTFIDYFMRKMNGDQIPSRPLISGSMQLILSIIRSIDFLEFRSSE 245

Query: 854 IAAAAILTAANEI 892
      IAA+ ++ + EI
Sbjct: 246 IAASVAMSVSGEI 258

>gi|3915637|sp|P42753|CGD3_ARATH CYCLIN DELTA-3 >gi|2995134|gnl|PID|e1284159 (X83371)
cyclin delta-3
      [Arabidopsis thaliana]
      Length = 376

Score = 186 bits (401), Expect(2) = 6e-46
Identities = 92/235 (39%), Positives = 143/235 (60%)

Query: 404 REESVGVILKVHAYYGFQPLTAYLAVNYMDRFLDSRRLPETNGWPLQLVSVACLSLAAKM 583
      R+E+VGWIL+V+A+YGF L A LA+ Y+D+F+ S L W LQLVSVACLSLAAK+
Sbjct: 87 RKEAVGWILRVNAHYGFSTLAAVLAITYLDKFICSYSLQDKPWMLQLVSVACLSLAAKV 146

Query: 584 EEPLVPSLLDLQIEGAKYIFEPRTIRRMELLVLGVLDWRLRSVTPLCFLAFFACKVDSTG 763
      EE VP LLD Q+E KY+FE +TI+RMELL+L L+W++ +TP+ F+ ++
Sbjct: 147 EETQVPLLLDFQVEETKYVFEAKTIQRMELLILSTLEWKMHLPISFVDHIIRRLGLKN 206

Query: 764 TFIRFLISRATEIIVSNIQEASFLAYWPSCIAAAAAILTAANEIPNWSVVKPENAESWCEG 943
      +++ ++S I ++ F+ Y PS +AAA ++ ++ + + +
Sbjct: 207 NAHWDFLNKCHRLLSVISDSRFVGYLPSVAAATMMRIIEQVDPFDPLSYQTNLLGVLN 266

Query: 944 LRKEKVIGCYQLMQELVIN 1000
      L KEKV CY L+ +L ++
Sbjct: 267 LTKEKVKTCYDLILQLPVD 285

Score = 20.8 bits (39), Expect(2) = 6e-46
Identities = 12/36 (33%), Positives = 19/36 (52%)

Query: 1022 LLKVLPLQLRVTTRTRMRSSSTVSSSSSSSTSFSLSC 1129
      L+ LP R+ + +++SS SSS+ S SC
Sbjct: 278 LILQLPVDRICLQIQSQSSKKRKS HDSSSSSLNSPSC 313

>gi|1076313|pir||S51652 cyclin delta-3 - Arabidopsis thaliana
Length = 376

Score = 186 bits (401), Expect(2) = 6e-46
Identities = 92/235 (39%), Positives = 143/235 (60%)

Query: 404 REESVGVILKVHAYYGFQPLTAYLAVNYMDRFLDSRRLPETNGWPLQLVSVACLSLAAKM 583
      R+E+VGWIL+V+A+YGF L A LA+ Y+D+F+ S L W LQLVSVACLSLAAK+
Sbjct: 87 RKEAVGWILRVNAHYGFSTLAAVLAITYLDKFICSYSLQDKPWMLQLVSVACLSLAAKV 146

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APPENDIX A (continued)

Query: 584 EEPLVPSLLDLQIEGAKYIFEPRTIRRMELLVLGVLDWRLRSVTPLCFLAFFACKVDSTG 763
 EE VP LLD Q+E KY+FE +TI+RMELL+L L+W++ +TP+ F+ ++
 Sbjct: 147 EETQVPLLLDFQVEETKYVFEAKTIQRMELLILSTLEWKMHLLITPISFVDHIIRRLGLKN 206

Query: 764 TFIRFLISRATEIIVSNIQEASFLAYWPSCIAAAAILTAANEIPNWSVVKPENAESWCEG 943
 +++ ++S I ++ F+ Y PS +AAA ++ ++ + + +
 Sbjct: 207 NAHWDFLNKCHRLLLSVISDSRFVGYLPSVAAATMMRIIEQVDPFDPLSYQTNLLGVLN 266

Query: 944 LRKEKVICYQLMQELVIN 1000
 L KEKV CY L+ +L ++
 Sbjct: 267 LTKEKVKTCYDLILQLPVD 285

Score = 20.8 bits (39), Expect(2) = 6e-46
 Identities = 12/36 (33%), Positives = 19/36 (52%)

Query: 1022 LLKVLPQLRVTTTRMRSSSTVSSFSSSSSTSFSLSC 1129
 L+ LP R+ + +++SS SSS+ S SC
 Sbjct: 278 LILQLPVDRICLQIQIQSSKKRKSHDSSSSLNSPSC 313

>gi|2911046|gnl|PID|e1253334 (AL021961) cyclin delta-3 [Arabidopsis thaliana]
 Length = 376

Score = 186 bits (401), Expect(2) = 8e-46
 Identities = 92/235 (39%), Positives = 143/235 (60%)

Query: 404 REESVGWILKVHAYYGFQPLTAYLAVNYMDRFLDSRRLPETNGWPLQLVSVACLSLAAKM 583
 R+E+VGWIL+V+A+YGF L A LA+ Y+D+F+ S L W LQLVSVACLSLAAK+
 Sbjct: 87 RKEAVGWILRVNAHYGFSTLAAVLAITYLDKFICSYSRLQDKPWWMLQLVSVACLSLAAKV 146

Query: 584 EEPLVPSLLDLQIEGAKYIFEPRTIRRMELLVLGVLDWRLRSVTPLCFLAFFACKVDSTG 763
 EE VP LLD Q+E KY+FE +TI+RMELL+L L+W++ +TP+ F+ ++
 Sbjct: 147 EETQVPLLLDFQVEETKYVFEAKTIQRMELLILSTLEWKMHLLITPISFVDHIIRRLGLKN 206

Query: 764 TFIRFLISRATEIIVSNIQEASFLAYWPSCIAAAAILTAANEIPNWSVVKPENAESWCEG 943
 +++ ++S I ++ F+ Y PS +AAA ++ ++ + + +
 Sbjct: 207 NAHWDFLNKCHRLLLSVISDSRFVGYLPSVAAATMMRIIEQVDPFDPLSYQTNLLGVLN 266

Query: 944 LRKEKVICYQLMQELVIN 1000
 L KEKV CY L+ +L ++
 Sbjct: 267 LTKEKVKTCYDLILQLPVD 285

Score = 20.3 bits (38), Expect(2) = 8e-46
 Identities = 12/36 (33%), Positives = 19/36 (52%)

Query: 1022 LLKVLPQLRVTTTRMRSSSTVSSFSSSSSTSFSLSC 1129
 L+ LP R+ + +++SS SSS+ S SC
 Sbjct: 278 LILQLPVDRIGLQIQIQSSKKRKSHDSSSSLNSPSC 313

>gi|1770190|gnl|PID|e290219 (Y10162) cyclin-D like protein [Chenopodium rubrum]
 Length = 372

Score = 80.8 bits (170), Expect(3) = 1e-45
 Identities = 92/221 (41%), Positives = 142/221 (63%)

Query: 314 IASFIEHERNFVPGFEYLSRFQSRSLDANAREESVGWILKVHAYYGFQPLTAYLAVNYMD 493
 +AS ++ER G +YL RF++ LD AR + WI KV ++Y F PL YL+VNY+D
 Sbjct: 79 LASLFDNERQHFLGLDYLKFRFRNGDLGLGARNLVIDWIHKVQSHYNGPLCVYLSVNYLD 138

Query: 494 RFLDSRRLP 520
 RFL + LP
 Sbjct: 139 RFLSAYELP 147

APPENDIX A (continued)

Score = 123 bits (264), Expect(3) = 1e-45
Identities = 60/152 (39%), Positives = 98/152 (64%)

Query: 533 WPLQLVSVACLSLAAKMEEPLVPSLLDLQIEGAKYIFEPRTIRRMELLVLGVLDWRLRSV 712
W +QL+ VACLSLAAK++E VP +LDLQ+ +K++FE +TI+RMELLVL L WR++SV
Sbjct: 151 WMMQLLGVACLSLAAKVDETDVPLILDQVSESKFVFEAKTIQRMELLVLSTLKWRMQSV 210

Query: 713 TPLCFLAFFACKVDSTGTGFIRFLISRATEIIVSNIQEASFLAYWPSCIAAAAILTAANE 889
TP F+ +F K+ + LI +A ++I+S I+ + + PS IAAA ++ +
Sbjct: 211 TPFSEFIDYFLYKLSGDKMPSKSLIFQAIQLILSTIKGIDLMEFRPSEIAAAVAISVTQQ 269

Score = 19.8 bits (37), Expect(3) = 1e-45
Identities = 7/33 (21%), Positives = 18/33 (54%)

Query: 944 LRKEKVIGCYQLMQELVINNNQRKLPLLKVLPQ 1042
+ KE+++ C ++M +L +++ +PQ
Sbjct: 287 VEKERLMKCVEIMHDLRMSSRSNGALASTSVPQ 319

>gi|1076312|pir||S51651 cyclin delta-2 - Arabidopsis thaliana
Length = 383

Score = 169 bits (364), Expect(3) = 8e-44
Identities = 96/232 (41%), Positives = 144/232 (61%)

Query: 314 IASFIEHERNFVPGFEYLSRFQSRSLDANAREESVGWILKVHAYYGFQPLTAYLAVNYMD 493
I + E F PG +Y+ R S LD + R +++ WILKV A+Y F L L++NY+D
Sbjct: 67 IKEMLVREIEFCPGTDYVKRLLSGDLDSVRNQALDWILKVCAHYHFGHLCICLSMNYLD 126

Query: 494 RFLDSRRLPETNGWPLQLVSVACLSLAAKMEEPLVPSLLDLQIEGAKYIFEPRTIRRMEL 673
RFL S LP+ W QL++V+CLSLA+KMEE VP ++DLQ+E K++FE +TI+RMEL
Sbjct: 127 RFLTSYELPKDKDWAQAQLLAVSCLSLASKMEETDVPHIVDLQVEDPKFVFEAKTIKRMEL 186

Query: 674 LVLGVLDWRLRSVTPLCFLAFFACKV 751
LV+ L+WRL+++TP F+ +F K+
Sbjct: 187 LVVTTLNWRLQALTPFSFIDYFVDKI 212

Score = 27.6 bits (54), Expect(3) = 8e-44
Identities = 27/86 (31%), Positives = 44/86 (50%)

Query: 779 LISRATEIIVSNIQEASFLAYWPSCIAAAAILTAA 883
LI R++ I++ + FL + PS IAAAA ++ +
Sbjct: 220 LIYRSSRFILNTTKAIEFLDFRPSEIAAAAVSVS 254

Score = 21.2 bits (40), Expect(3) = 8e-44
Identities = 14/51 (27%), Positives = 22/51 (42%)

Query: 860 AAAAILTAANEIPNWSVVKPENAESWCEGLRKEKVIGCYQLMQELVINNNQR 1012
AAA + + + E A S +++E+V C LM+ L N R
Sbjct: 246 AAAAVSVSISGETECIDEEKALSSLIYVKQERVKRCNLNMRSLTGEENVR 296

Rb-binding
LXCXE

SEQ ID NO:12 (amended)	1	MNAEPLPPALLMSVCLSDYDLLCGEDSSGILSGESP-ECSFSDIDSSPPPPSPPTTDC	1	MRSYR-FSDYLHMSVFSNDMDLFCGEDS-GVFSGESTVDFFSSEVDSWPGD-----	MNAE--SPPG	[1=====Region A=====60]
SEQ ID NO:12 (amended)	60	YSIASFIEHERNFVPGFEYLSRFQSRSLDANAREESVGWILKVHAYYGFQPLTAYLAVNY	51	-SIACFIEDERHFVPGHDYLSRFQTRSLDASAREDSVAWILKVQAYYNFQPLTAYLAVNY	[61=====Region B=====120	
SEQ ID NO:12 (amended)	120	MDRFLDSRRLPETNGWPLQLVSVACLSLAAKMEEPVPSLLDLQIEGAKYIFEPRTIRRM	110	MDRFLYARRLPETSGWPMQLLAVACLSLAAKMEEILVPSLDFQVAGVKYLFEAKTIKRM	121=====Region B=====180	
SEQ ID NO:12 (amended)	180	ELLVLGVLDWRLRSVTPLCFLAFFACKVDSTGTFRFLISRATEIIVSNIQEASFLAYWP	170	ELLVLSVDWRLRSVTPFDFFISFFAYKIDPSGTFGLFFISHATEIILSNIKEASFLEYWP	181=====Region B=====240	
SEQ ID NO:12 (amended)	240	SCIAAAAILTAANEIPNWS-VVKP-ENAESWCEGLRKEKVIGCYQLMQELVINNNQRKLP	230	SSIAAAAILCVANELPSLSSVNPHEPETHWCDGLSKEKIVRCYRLMKAMAIENN--RLN	241===B===] [=====Region C=====300	
SEQ ID NO:12 (amended)	298	LLKVLPQLRVTTTRMRSSSTVSSSSSTSFSLSCKRRKLNRLWV-DDKGNSE	288	TPKVIAKLRSVRA--SSTLTRPSDESSP---CKRRKLSGYSWVGDETSTN	301=====Region C=====355]	

APPENDIX C

>gi|3915635|sp|P42751|CGD1_ARATH CYCLIN DELTA-1 >gi|2995130|gnl|PID|e1284155 (X83369) cyclin delta-1
[Arabidopsis thaliana]
Length = 335

Score = 38.2 bits (77), Expect(4) = e-115
Identities = 199/307 (64%), Positives = 239/307 (77%)

Query: 161 LLMSVSLSDYDLLCGEDSSGILSGESPECSFSDIDSSP 277
L MSVS +D DL CGEDS + + S S++DS P
Sbjct: 10 LHMSVSFSNDMDLFCGEDSGVFSGESTVDFSSSEVDSWP 48

Score = 357 bits (774), Expect(4) = e-115
Identities = 181/268 (67%), Positives = 216/268 (80%)

Query: 311 SIASFIEHERNFVPGEYLSRFQSRSLDANAREESVGWILKVHAYYGFQPLTAYLAVNYM 490
SIA FIE ER+FVPG +YLSRFQ+RSLDA+ARE+SV WILKV AYY FQPLTAYLAVNYM
Sbjct: 51 SIACFIEDERHFVPGHDYLSRFQTRSLDASAREDSVAWILKVQAYYNFQPLTAYLAVNYM 110

Query: 491 DRFLDSRRLPETNGWPLQLVSVACLSLAAKMEEPLVPSLLDLQIEGAKYIFEPTIRRM 670
DRFL +RRLPET+GWP+QL++VACLSLAAKMEE LVPSL D Q+ G KY+FE +TI+RME
Sbjct: 111 DRFLYARRLPETSGWPMQLLAVACLSLAAKMEEILVPSLDFQVAGVKYLF EAKTIKRME 170

Query: 671 LLVLGVLDWRLRSVTPLCFLAFFACKVDSTGTFFIRFLISRATEIIVSNIQEASFLAYWPS 850
LLVL VLDWRLRSVTP F++FEA K+D +GTF+ F IS ATEII+SNI+EASFL YWPS
Sbjct: 171 LLVLSVLDWRLRSVTPPDFISFFAYKIDPSGTFLGFFISHATEIILSNIKEASFLEYWPS 230

Query: 851 CIAAAAILTAANEIPNWSVV 910
IAAAAIL ANE+P+ S V
Sbjct: 231 SIAAAAILCVANELPSLSSV 250

APPENDIX C (continued)

Score = 53.3 bits (110), Expect(4) = e-115
Identities = 31/68 (45%), Positives = 43/68 (62%)

Query: 917 ENAESWCEGLRKEKVGICYQLMQELVINNNQRKLP 1021
E+ E+WC+GL KEK++ CY+LM+ + I NN+ P
Sbjct: 255 ESPETWCDGLSKEKIVRCYRLMKAMAIENNRNLTP 289

Score = 29.0 bits (57), Expect(4) = e-115
Identities = 14/33 (42%), Positives = 17/33 (51%)

Query: 1073 SSTVSSFSSSSSTSFSLCKRRKLNRLWVDDK 1171
S SS + S S CKRRKL+ WV D+
Sbjct: 298 SVRASSTLTRPSDESSSPCKRRKLSGYSWGDE 330